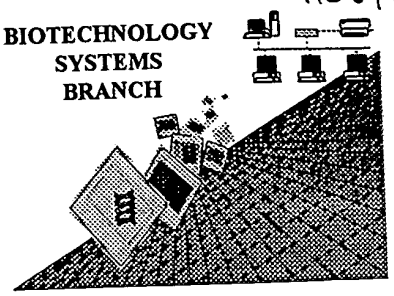
#8 CRF
09/28/99

Lundgren

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/301,704A

Art Unit / Team No. : 1653

Date Processed by STIC: 8/26/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION SERIAL NUMBER: 09/301,704A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 ____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 ____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 ____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 ____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 ____ Variable Length
Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 ____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.

8 ____ Skipped Sequences (OLD RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 ____ Skipped Sequences (NEW RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 ✓ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 ____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 ✓ Use of <220>Feature (NEW RULES)
Sequence(s) 2-7 are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 ____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

AKS-Biotechnology Systems Branch- 5/15/99

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/301,704A

DATE: 08/26/1999
TIME: 11:01:29

Input Set: I301704A.RAW

This Raw Listing contains the General Information Section and up to first 5 pages.

RR 5,12-3

<110> APPLICANT: Schembri, Mark Andrew
Klemm, Per
<120> TITLE OF INVENTION: Novel multifunctional adhesin proteins and their display in microbial cells
<130> FILE REFERENCE: 21352 PC 1
<140> CURRENT APPLICATION NUMBER: US/09/301,704A
<141> CURRENT FILING DATE: 1999-04-29
<150> EARLIER APPLICATION NUMBER: PA 1998 00598
<151> EARLIER FILING DATE: 1998-04-30
<160> NUMBER OF SEQ ID NOS: 46
<170> SOFTWARE: FastSEQ for Windows Version 3.0

Does Not Comply
Corrected Diskette Needed

<210> SEQ ID NO 1
<211> LENGTH: 300
<212> TYPE: PRT
<213> ORGANISM: E. coli PC31 FimH
<400> SEQUENCE: 1

Met Lys Arg Val Ile Thr Leu Phe Ala Val Leu Leu Met Gly Trp Ser
1 5 10 15
Val Asn Ala Trp Ser Phe Ala Cys Lys Thr Ala Asn Gly Thr Ala Ile
20 25 30
Pro Ile Gly Gly Gly Ser Ala Asn Val Tyr Val Asn Leu Ala Pro Val
35 40 45
Val Asn Val Gly Gln Asn Leu Val Val Asp Leu Ser Thr Gln Ile Phe
50 55 60
Cys His Asn Asp Tyr Pro Glu Thr Ile Thr Asp Tyr Val Thr Leu Gln
65 70 75 80
Arg Gly Ser Ala Tyr Gly Gly Val Leu Ser Asn Phe Ser Gly Thr Val
85 90 95
Lys Tyr Ser Gly Ser Ser Tyr Pro Phe Pro Thr Thr Ser Glu Thr Pro
100 105 110
Arg Val Val Tyr Asn Ser Arg Thr Asp Lys Pro Trp Pro Val Ala Leu
115 120 125
Tyr Leu Thr Pro Val Ser Ser Ala Gly Gly Val Ala Ile Lys Ala Gly
130 135 140
Ser Leu Ile Ala Val Leu Ile Leu Arg Gln Thr Asn Asn Tyr Asn Ser
145 150 155 160
Asp Asp Phe Gln Phe Val Trp Asn Ile Tyr Ala Asn Asn Asp Val Val
165 170 175
Val Pro Thr Gly Gly Cys Asp Val Ser Ala Arg Asp Val Thr Val Thr
180 185 190
Leu Pro Asp Tyr Pro Gly Ser Val Pro Ile Pro Leu Thr Val Tyr Cys
195 200 205
Ala Lys Ser Gln Asn Leu Gly Tyr Tyr Leu Ser Gly Thr His Ala Asp
210 215 220

```
45          Ala Gly Asn Ser Ile Phe Thr Asn Thr Ala Ser Phe Ser Pro Ala Gln
46          225                 230                 235                 240
47          Gly Val Gly Val Gln Leu Thr Arg Asn Gly Thr Ile Ile Pro Ala Asn
48                              245                 250                 255
49          Asn Thr Val Ser Leu Gly Ala Val Gly Thr Ser Ala Val Ser Leu Gly
50                          260                 265                 270
51          Leu Thr Ala Asn Tyr Ala Arg Thr Gly Gly Gln Val Thr Ala Gly Asn
52                      275                 280                 285
53          Val Gln Ser Ile Ile Gly Val Thr Phe Val Tyr Gln
54              290                 295                 300
55      <210> SEQ ID NO 2
56      <211> LENGTH: 7
57      <212> TYPE: PRT
58      <213> ORGANISM: Artificial Sequence
59      <220> FEATURE:
60      <221> NAME/KEY: BINDING
61      <222> LOCATION: 2..4
62      <223> OTHER INFORMATION: Binding motif for binding metal oxides
63      <400> SEQUENCE: 2
W--> 64         His Xaa Xaa Xaa His Arg Ser
65               1               5
66      <210> SEQ ID NO 3
67      <211> LENGTH: 7
68      <212> TYPE: PRT
69      <213> ORGANISM: Artificial Sequence
70      <220> FEATURE:
71      <221> NAME/KEY: BINDING
72      <222> LOCATION: 2..4
73      <223> OTHER INFORMATION: Binding motif for binding metal oxides
74      <400> SEQUENCE: 3
W--> 75         Arg Xaa Xaa Xaa His Arg Ser
76               1               5
77      <210> SEQ ID NO 4
78      <211> LENGTH: 7
79      <212> TYPE: PRT
80      <213> ORGANISM: Artificial Sequence
81      <220> FEATURE:
82      <221> NAME/KEY: BINDING
83      <222> LOCATION: 3..4
84      <223> OTHER INFORMATION: Binding motif for binding metal oxides
85      <400> SEQUENCE: 4
W--> 86         Ser Lys Xaa Xaa His Arg Ser
87               1               5
88      <210> SEQ ID NO 5
89      <211> LENGTH: 7
90      <212> TYPE: PRT
91      <213> ORGANISM: Artificial Sequence
92      <220> FEATURE:
93      <221> NAME/KEY: BINDING
94      <222> LOCATION: 3..4
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all item 12 on Error Summary Sheet

all item 10 on Error Summary Sheet

item 12

item 10

item 12

item 10

item 12

<223> OTHER INFORMATION: Binding motif for binding metal oxides
<400> SEQUENCE: 5
W--> **Ser Arg Xaa Xaa His Arg Ser**
1 5
<210> SEQ ID NO 6
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: BINDING
<222> LOCATION: 3..4
<223> OTHER INFORMATION: Binding motif for binding metal oxides
<400> SEQUENCE: 6
W--> **Thr Lys Xaa Xaa His Arg Ser**
1 5
<210> SEQ ID NO 7
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: BINDING
<222> LOCATION: 3..4
<223> OTHER INFORMATION: Binding motif for binding metal oxides
<400> SEQUENCE: 7
W--> **Thr Arg Xaa Xaa His Arg Ser**
1 5
<210> SEQ ID NO 8
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide for the construction of a double-stranded poly histidine segment (Example 1)
<400> SEQUENCE: 8
gatctcatca ccatcatcac catg 24
<210> SEQ ID NO 9
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide for the construction of a double-stranded poly histidine segment (Example 1)
<400> SEQUENCE: 9
gatccatggt gatgatggtg atga 24
<210> SEQ ID NO 10
<211> LENGTH: 54
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: unsure

<222> LOCATION: 13..39
<223> OTHER INFORMATION: v indicates equal molar amounts of A, C, and G;and
n indicates equal molar amounts of A, C, T, G in
template oligonucleotide
<400> SEQUENCE: 10
ggacgcagat ctvnnnvnnvn nvnnnvnnvnn vnnvnnnvnna gatctagcac cagt 54

W--> 10

<210> SEQ ID NO 11
<211> LENGTH: 15
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer oligonucleotide
<400> SEQUENCE: 11
actggtgcta gatct 15

<210> SEQ ID NO 12
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Sequence conferring the ability of cells to adhere
to metal oxides
<400> SEQUENCE: 12
Arg Ser Val Val Arg Pro Lys Ala Ala Thr Asn Arg Ser
1 5 10

<210> SEQ ID NO 13
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Sequence conferring the ability of cells to adhere
to metal oxides
<400> SEQUENCE: 13
Arg Ser Arg Ile Arg His Arg Leu Val Gly Gln Arg Ser
1 5 10

<210> SEQ ID NO 14
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Sequence conferring the ability of cells to adhere
to metal oxides
<400> SEQUENCE: 14
Arg Ser Val Lys Asp Gly Ser Ala Thr Ala Lys Arg Ser Val Ala Asn
1 5 10 15
Phe Glu Thr Pro Arg Val Arg Ser
20

<210> SEQ ID NO 15
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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195  <220> FEATURE:
196  <223> OTHER INFORMATION: Sequence conferring the ability of cells to adhere
197        to metal oxides
198  <400> SEQUENCE: 15
199        Arg Ser Ala Pro Gln Thr Gly Arg Pro Asn Asn Arg Ser Leu Pro Leu
200         1               5                  10                  15
201        Gly Asn Arg Asp Met Gln Arg Ser
202                    20
203  <210> SEQ ID NO 16
204  <211> LENGTH: 13
205  <212> TYPE: PRT
206  <213> ORGANISM: Artificial Sequence
207  <220> FEATURE:
208  <223> OTHER INFORMATION: Sequence conferring the ability of cells to adhere
209        to metal oxides
210  <400> SEQUENCE: 16
211        Arg Ser Val Gln Asn Asp Arg Ile Val Ala Gly Arg Ser
212         1               5                  10
213  <210> SEQ ID NO 17
214  <211> LENGTH: 13
215  <212> TYPE: PRT
216  <213> ORGANISM: Artificial Sequence
217  <220> FEATURE:
218  <223> OTHER INFORMATION: Sequence conferring the ability of cells to adhere
219        to metal oxides
220  <400> SEQUENCE: 17
221        Arg Ser Tyr Pro Pro Phe His Asn Asn Asp His Arg Ser
222         1               5                  10
223  <210> SEQ ID NO 18
224  <211> LENGTH: 24
225  <212> TYPE: PRT
226  <213> ORGANISM: Artificial Sequence
227  <220> FEATURE:
228  <223> OTHER INFORMATION: Sequence conferring the ability of cells to adhere
229        to metal oxides
230  <400> SEQUENCE: 18
231        Arg Ser Asn Thr Arg Met Thr Ala Arg Gln His Arg Ser Ala Asn His
232         1               5                  10                  15
233        Lys Ser Thr Gln Arg Ala Arg Ser
234                    20
235  <210> SEQ ID NO 19
236  <211> LENGTH: 24
237  <212> TYPE: PRT
238  <213> ORGANISM: Artificial Sequence
239  <220> FEATURE:
240  <223> OTHER INFORMATION: Sequence conferring the ability of cells to adhere
241        to metal oxides
242  <400> SEQUENCE: 19
243        Arg Ser Leu Ala Ile Asp Gly Thr Asp Val Gln Arg Ser Lys Pro Leu
244         1               5                  10                  15
```

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

IFYI

VERIFICATION SUMMARY
PATENT APPLICATION US/09/301,704A

DATE: 08/26/1999
TIME: 11:01:29

Input Set: I301704A.RAW

Line	?	Error/Warning	Original Text
64	W	"N" or "Xaa" used: Feature required	His Xaa Xaa Xaa His Arg Ser
75	W	"N" or "Xaa" used: Feature required	Arg Xaa Xaa Xaa His Arg Ser
86	W	"N" or "Xaa" used: Feature required	Ser Lys Xaa Xaa His Arg Ser
97	W	"N" or "Xaa" used: Feature required	Ser Arg Xaa Xaa His Arg Ser
108	W	"N" or "Xaa" used: Feature required	Thr Lys Xaa Xaa His Arg Ser
119	W	"N" or "Xaa" used: Feature required	Thr Arg Xaa Xaa His Arg Ser
150	W	"N" or "Xaa" used: Feature required	ggacgcagat ctvnnvnnvn nvnnvnnvnn vnnvnnvn
416	W	"N" or "Xaa" used: Feature required	Ser Lys Xaa Xaa Ala Arg
427	W	"N" or "Xaa" used: Feature required	Ser Arg Xaa Xaa Ala Arg
438	W	"N" or "Xaa" used: Feature required	Thr Lys Xaa Xaa Ala Arg
449	W	"N" or "Xaa" used: Feature required	Thr Arg Xaa Xaa Ala Arg
460	W	"N" or "Xaa" used: Feature required	Arg Xaa Xaa Xaa His Arg Ser